

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/591,632 B  
Source: IFW/16  
Date Processed by STIC: 12/8/05

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)**
- 2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450**
- 3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**  
**U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314**

Revised 01/24/05

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER:

09/591,632 B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics    The number/text at the end of each line "wrapped" down to the next line. This may occur if your file  
     Wrapped Aminos        was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will  
                               prevent "wrapping."
  
- 2      Invalid Line Length    The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
  
- 3      Misaligned Amino        The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers;  
     Numbering                use **space characters**, instead.
  
- 4      Non-ASCII                The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. Please  
                               **ensure your subsequent submission is saved in ASCII text.**
  
- 5      Variable Length        Sequence(s)      contain n's or Xaa's representing more than one residue. **Per Sequence Rules,**  
                               **each n or Xaa can only represent a single residue.** Please present the **maximum** number of each  
                               residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6 ✓ PatentIn 2.0                A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
     "bug"                      sequences(s) 15,17,40. Normally, PatentIn would automatically generate this section from the  
                               previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to  
                               the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for**  
                               **Artificial or Unknown sequences.**
  
- 7      Skipped Sequences      Sequence(s)      missing. If intentional, please insert the following lines for **each** skipped sequence:  
     (OLD RULES)                (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                     (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                                     (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                     This sequence is intentionally skipped  
  
                               Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
  
- 8      Skipped Sequences      Sequence(s)      missing. If **intentional**, please insert the following lines for **each** skipped sequence.  
     (NEW RULES)                <210> sequence id number  
                                     <400> sequence id number  
                                     000
  
- 9      Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
     (NEW RULES)                Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.  
                                     In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
  
- 10      Invalid <213>            Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or  
     Response                    scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or  
                                     is Artificial Sequence
  
- 11      Use of <220>            Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
                                     Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or  
                                     "Unknown." Please explain source of genetic material in <220> to <223> section.  
                                     (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12      PatentIn 2.0            Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,  
     "bug"                      resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence  
                                     listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
  
- 13      Misuse of n/Xaa        "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFW16

## RAW SEQUENCE LISTING

DATE: 12/08/2005

PATENT APPLICATION: US/09/591,632B

TIME: 09:37:52

Input Set : A:\34978a.txt

Output Set: N:\CRF4\12082005\I591632B.raw

4 <110> APPLICANT: Lindquist, Susan  
 5 Li, Liming  
 6 Ma, Jiyan  
 7 Liu, Jia-Jia  
 8 Sondheimer, Neal  
 9 Scheibel, Thomas  
 11 <120> TITLE OF INVENTION: RECOMBINANT PRION-LIKE GENES AND PROTEINS AND MATERIALS  
 12 AND METHODS COMPRISING SAME  
 14 <130> FILE REFERENCE: 30554/34978A  
 16 <140> CURRENT APPLICATION NUMBER: 09/591,632B  
 17 <141> CURRENT FILING DATE: 2000-06-09  
 19 <150> PRIOR APPLICATION NUMBER: US 06/138,833 → 60/138,833  
 20 <151> PRIOR FILING DATE: 1999-06-09  
 E--> 22 <160> NUMBER OF SEQ ID NOS: 65 ← 70 (p. 2)  
 24 <170> SOFTWARE: PatentIn Ver. 2.0

## ERRORED SEQUENCES

↓  
 This version of PatentIn  
 has bugs. (see item 6  
 on Error Summary  
 sheet)

Does Not Comply  
 corrected Diskette Needs

Suggestion: use a more  
 recent version  
 of PatentIn.

You can download  
 PatentIn 3.3 (at no  
 charge) from the USPTO  
 website  
[www.uspto.gov](http://www.uspto.gov)

<210> 70 last sequence in submitted file  
<211> 286  
<212> PRT  
<213> Saccharomyces cerevisia

<400> 70

Met Ser Ile Gln His Phe Arg Val Ala Leu Ile Pro Phe Phe Ala Ala  
1 5 10 15

see pp 3-4-5  
for more  
errors

3

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/591,632B

DATE: 12/08/2005  
TIME: 09:37:54

Input Set : A:\34978a.txt  
Output Set: N:\CRF4\12082005\I591632B.raw

Use of <220> Feature(NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223>

section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32)

(Sec.1.823 of new Rules)

Seq#:15,17,40

↓  
see p.4 for sample

This is due to Patent In 2.0 bug  
(see item 6 on Error  
summary  
sheet)

09/591,632B 4

<210> 15

<211> 215

<212> PRT

<213> Artificial Sequence

↙ no 42207-42237 section

<400> 15

Met Ser Asp Ser Asn Gln Gly Asn Asn Gln Gln Asn Tyr Gln Gln Tyr  
1 5 10 15

09/59/632B 5

(from the end of sequence 3)

ggt gaa tga aggctgcttt aaaaacaaga aagaaagaag aaggaggaaa  
Gly Glu

1286

355 delete this, since no amino acid is shown under the stop

agaagggttat aagggtatgt atataggcag aaaaaagga aaattaagtg caaatataaa 1346

codon

caaaaatgtc atagaagtat ataatagttt tgaaatttct gttgcttcta ttatttcitt 1406

(+ga)

gttaccctcaa ccacagaatt c

1427

**VERIFICATION SUMMARY**

DATE: 12/08/2005

PATENT APPLICATION: US/09/591,632B

TIME: 09:37:54

Input Set : A:\34978a.txt

Output Set: N:\CRF4\12082005\I591632B.raw

L:497 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:803 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:15, <213>  
ORGANISM:Artificial Sequence  
L:803 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:15, <213>  
ORGANISM:Artificial Sequence  
L:803 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:803  
L:935 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:17, <213>  
ORGANISM:Artificial Sequence  
L:935 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:17, <213>  
ORGANISM:Artificial Sequence  
L:935 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:17,Line#:935  
L:2954 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:39  
L:2962 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:40, <213>  
ORGANISM:Artificial Sequence  
L:2962 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:40, <213>  
ORGANISM:Artificial Sequence  
L:2962 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:40,Line#:2962  
L:22 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (65) Counted (70)